10081806.060702

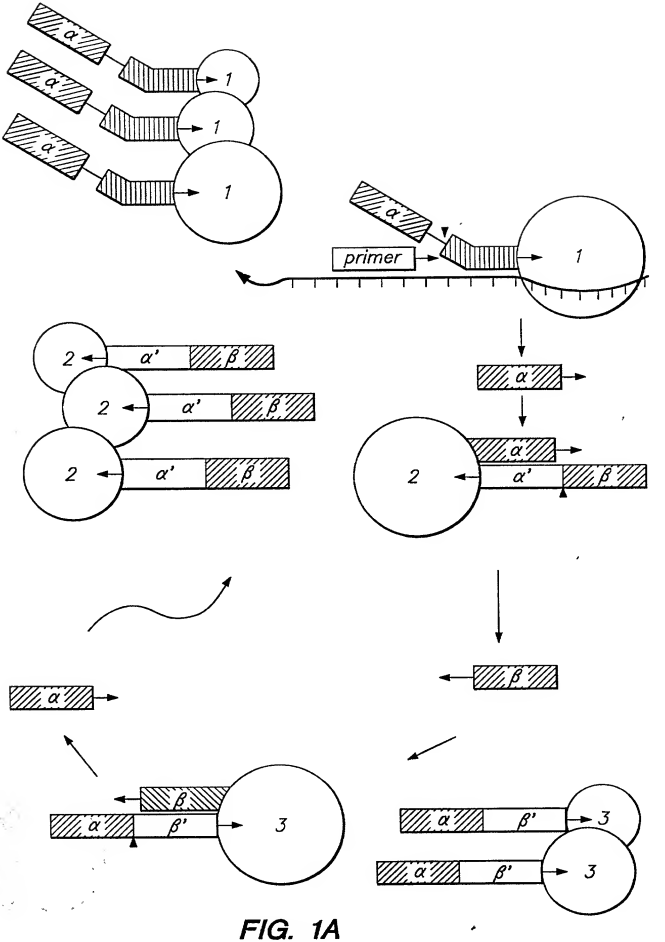


FIG. 1A

20050080702

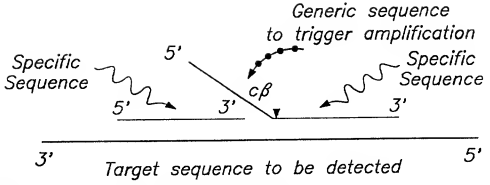


FIG. 1B *PART ONE: TRIGGER REACTION*

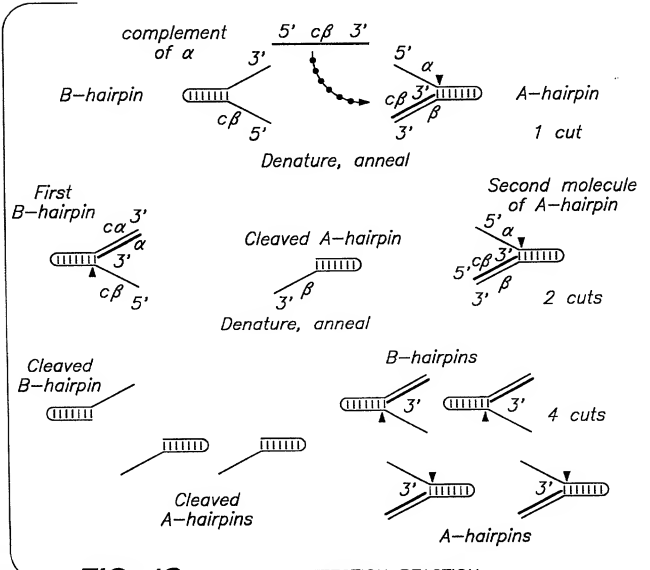


FIG. 1C *PART TWO: DETECTION REACTION*

20/090 '90818001

```
MAJORITY ATGXXGGCGATGCTTCCCCTCTTTGAGCCCAAAGGCCGGGTCCTCCTGGTGGACGGGCACCACCTGGCCT

DNAPTAQ  ...AG..G......G.................G..................................... 70
DNAPTFL  ..................................C..G..................................... 67
DNAPTTH  ...GA............G........A.......................................... 70

MAJORITY ACCGCACCTTCTTCGCCCTGAAGGGCCTCACCACCACCOGGGGGGAACCGGTGCAGGCGGTCTACGGCTT

DNAPTAQ  ..........CA.............................G..G..................... 140
DNAPTFL  ............T.....C.....................C........C..T.............. 137
DNAPTTH  ................................G.................................... 140

MAJORITY CGCCAAGAGCCTCCTCAAGGCCCTGAAGGAGGACGGGGACXXGCCGGTGXTCGTGGTCTTTGACGCCAAG

DNAPTAQ  ........................C.........................A..................... 207
DNAPTFL  ......A.................................GT..T.......................... 204
DNAPTTH  ..................................T..AA...C..CT..................... 280

MAJORITY GCCCCCTCCTTCCGCCACGAGGCCTACGAGGCCTACAAGGCGGGCCGGGCCCCCACCCCGGAGGACTTTC

DNAPTAQ  ..........................G..GG.....................G.............. 277
DNAPTFL  ..................................................................... 274
DNAPTTH  ..........................................GA.......G.....C.........C. 280

MAJORITY CCCGGCAGCTCGCCCTCATCAAGGAGCTGGTGGACCTCCTGGGGCTTGCGCGCCTCGAGGTCCCCGGCTA

DNAPTAQ  .......A.....................................G.................G..... 347
DNAPTFL  ..........G..............T.............A..C....T...G..G.....T.......T 344
DNAPTTH  ..........................................T..A.C..................... 350
```

FIG. 2A

```
MAJORITY CGAGGCGGACGACGTXCTGGCCACCCTGGCCAAGAAGGCGGAAAAGGAGGGGTACGAGGTGCGCATCCTC

DNAPTAQ  ...............C.......G...........................C........C.........  417
DNAPTFL  T..............G..................CG..................................  414
DNAPTTH  ...............T..C...................................................  420

MAJORITY ACCGCCGACCGCGACCTCTACCAGCTCCTTTCCGACCGCATCGCCGTCCTCCACCCCGAGGGGTACCTCA

DNAPTAQ  .........AAA.....T........................CA..........................  487
DNAPTFL  ..T.............................G..G.........A..........T...........G.  484
DNAPTTH  .......................A...G.C.........G.......................CC.....  490

MAJORITY TCACCCCGGCGTGGCTTTGGGAGAAGTACGGCCTGAGGCCGGAGCAGTGGGTGGACTACCGGGCCCTGGC

DNAPTAQ  ..........C...........A.................C..C........CC..............A.  557
DNAPTFL  ..................AC...............C.C................................  554
DNAPTTH  .........A........................C......................T...C.....C.T  560

MAJORITY GGGGGACCCCTCCGACAACCTCCCCGGGGTCAAGGGCATCGGGGAGAAGACCGCCCXGAAGCTCCTCXAG

DNAPTAQ  C......GAG...........T.............................G..GAG......T..GG..  627
DNAPTFL  ............G..T...A..........G.........................A..G....A..CGC  624
DNAPTTH  ........................................................TC.........A..  630

MAJORITY GAGTGGGGGAGCCTGGAAAACCTCCTCAAGAACCTGGACCGGGTGAAGCCCGC...CXTCCGGGAGAAGA

DNAPTAQ  ..................GC......................C..............A............  694
DNAPTFL  ........................T..C..C.........A..........T.....T.G.........C  691
DNAPTTH  ........A...................................A.....A.AAAA.G............  700
```

FIG. 2B

20709D 90818001

```
MAJORITY TCCAGGCCCACATGGAXGACCTGAXGCTCTCCTGGGAGCTXTCCCAGGTGCGCACCGACCTGCCCCTGGA

DNAPTAQ  ...T.....C..T....A.....C..GG..A..... 764
DNAPTFL  ....G.GGG......G.C....GCC..T...C..A....T.....A...T..... 761
DNAPTTH  ..A.....C....A.....C.G.....T......C....G.....C..... 770

MAJORITY GGTGGACTTCGCCAAGXGGCGGGAGCCCGACCGGGAGGGGCTTAGGGCCTTTCTGGAGAGGCTGGAGTTT

DNAPTAQ  .....AA.....A.....T..... 834
DNAPTFL  .....GG.G.C.C..CACA...A...T......T..GC....T...T.....C..T..... 831
DNAPTTH  .....C.....C..G.....C.....C 840

MAJORITY GGCAGCCTCCTCCACGAGTTCGGCCTCCTGGAGGGCCCCAAGGCCCTGGAGGAGGCCCCCTGGCCCCCGC

DNAPTAQ  .....T.....AA..... 904
DNAPTFL  ..A.....G..G.....GGCA.....T. 901
DNAPTTH  .....C....GCCC..... 910

MAJORITY CGGAAGGGGCCTTCGTGGGCTTTGTCCTTTCCCGCCCCGAGCCCATGTGGGCCGAGCTTCTGGCCCTGGC

DNAPTAQ  .....G.....AAG.....T..... 974
DNAPTFL  .....T..TT.....TC.T.....T..... 971
DNAPTTH  .....C.....C.....G.....AAA..... 980

MAJORITY CGCCGCCAGGGAGGGCCGGGTCCACCGGGCACCAGACCCCTTTAXGGGCCTXAGGGACCTXAAGGAGGTG

DNAPTAQ  .....G.....C..C..G..T.A..AA.C...C.....G.....C. 1044
DNAPTFL  T.GG..GT.....G..CC....T.....A.....C...G.....G.....T....G.... 1041
DNAPTTH  ....TG.....C.....G.....G.....GGC...G..A.A.....C.....C 1050
```

FIG. 2C

```
MAJORITY CGGGGXCTCCTCGCCAAGGACCTGGCCGTTTTGGCCCTGAGGGAGGGCCTXGACCTCXTGCCCGGGGACG

DNAPTAQ  .....G..T.........A......AG....C.............A.....T.G....CC......C.... 1114
DNAPTFL  .....AA....G..............G.............C..........G......T.C..A.A..... 1111
DNAPTTH  .....C.................C.....C......TC.........G..A......G............ 1120

MAJORITY ACCCCATGCTCCTCGCCTACCTCCTGGACCCCTCCAACACCACCCCCGAGGGGGTGGCCCGGCGCTACGG

DNAPTAQ  ................................T..................................... 1184
DNAPTFL  ...........G..........T.......................T.................T..... 1181
DNAPTTH  ..................................................G.......... 1190

MAJORITY GGGGGAGTGGACGGAGGAXGCGGGGGAGCGGGCCCTCCTXTCCGAGAGGCTCTTCCXGAACCTXXXGGAG

DNAPTAQ  C.................G..............GC...T..............GCC.....GTG..G. 1254
DNAPTFL  .................T.........A..........GG.....C.C.......A..C...AAA.... 1260
DNAPTTH  .................C..C.CCC.C..........C..G.........CAT.G......CCTTA.. 1260

MAJORITY CGCCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACCAGGAGGTGGAGAAGCCCCTTTCCCGGGTCCIGG

DNAPTAQ  A.G.....................................G..........G..........GCT....... 1324
DNAPTFL  ......A....A..A..AC.C..G.............G..............G...........GT... 1321
DNAPTTH  .....C.............A............C.....C.........A........C............. 1330

MAJORITY CCCACATGGAGGCCACGGGGGTXCGGCTGGACGTGGCCTACCTCCAGGCCCTXTCCCTGGAGGTGGCGGA

DNAPTAQ  ......................G..C.............T...AG....T.G.............C.. 1394
DNAPTFL  ...GG.................C.............................C.............A..C 1391
DNAPTTH  ...............C.....A.....................T.........T.........C.T..... 1400
```

FIG.2D

20/090'90818001

```
MAJORITY GGAGATCCGCCGCCTCGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGGGAC

DNAPTAQ  .......GC...........CC.................................................. 1464
DNAPTFL  ....G.G....AG..G.....................................................C... 1461
DNAPTTH  ................................T....G..................................... 1470

MAJORITY CAGCTGGAAAGGGTGCTCTTTGACGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGAAGACXGGCAAGC

DNAPTAQ  .............C.............A.....................................C....... 1534
DNAPTFL  ........GC.................G..C..G..T.....................G..G..A. 1531
DNAPTTH  ..........................TA..........T.G..G......C.A.....A....... 1540

MAJORITY GCTCCACCAGCGCCGCCGTGCTGGAGGCCCTXCGXGAGGCCCACCCCATCGTGGAGAAGATCCTGCAGTA

DNAPTAQ  ..................C...........C..C.................................... 1604
DNAPTFL  .............T.................G..A.....................CCGC........... 1601
DNAPTTH  ................G...............A..G.....................................C...C. 1610

MAJORITY CCGGGAGCTCACCAAGCTCAAGAACACCTACATXGACCCCCTGCCXGXCCTCGTCCACCCCAGGACGGGC

DNAPTAQ  .................G....G.........T......T....G.A....A.................. 1674
DNAPTFL  ................................A...........C.C...G..........A...C... 1671
DNAPTTH  ..............................G.G...........AAG............G......... 1680

MAJORITY CGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTTAGTAGCTCCGACCCCAACCTGC

DNAPTAQ  ..............................................A...........T........C. 1744
DNAPTFL  ..G..........................C..............TCC..................... 1741
DNAPTTH  .....................................G.......................... 1750
```

FIG. 2E

```
MAJORITY AGAACATCCCCGTCCGCACCCCXCTGGGCCAGAGGATCCGCCGGGCCTTCGTGGCCGAGGAGGGXTGGGT

DNAPTAQ  .....................G..T..G.....................A.C...........G...C. 1814
DNAPTFL  .............G........T.........C.C........A.....................C..... 1811
DNAPTTH  .....................CT.....................................C...T....C 1820

MAJORITY GTTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCCTGGCCCACCTCTCCGGGGACGAGAACCTG

DNAPTAQ  A.....................................A....G.................C.............. 1884
DNAPTFL  .C......T.T.......C.........T.....T..................................... 1881
DNAPTTH  .....................................C.....C.....................A...... 1890

MAJORITY ATCCGGGTCTTCCAGGAGGGGAGGGACATCCACACCCAGACCGCCAGCTGGATGTTCGGCGTCCCCCCGG

DNAPTAQ  .....................C.............GG.................................G.. 1954
DNAPTFL  ...........T.....................................................TT....C. 1951
DNAPTTH  ...A..................A.....................A.......................... 1960

MAJORITY AGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCGGGGTCCTCTACGGCATGTCGGC

DNAPTAQ  .....................................................................G.. 2024
DNAPTFL  .A.GG..A.....T.....................................G.................... 2021
DNAPTTH  .....................................GG.G.........C..................... 2030

MAJORITY CCACCGCCTCTCCCAGGAGCTTGCCATCCCCTACGAGGAGGCGGTGGCCTTCATTGAGCGCTACTTCCAG

DNAPTAQ  .....................A.........T...........CCA.....................T... 2094
DNAPTFL  .............GG.......T..................................................... 2091
DNAPTTH  ...TA.G.....................................................T..A.............A 2100
```

FIG. 2F

```
MAJORITY AGCTTCCCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGTACGTGGAGA

DNAPTAQ  ......................................................................  2164
DNAPTFL  ....A........................GG.......C.........C.CC..........T.......  2161
DNAPTTH  ..........................A..A.................G....A......C........A.  2170

MAJORITY CCCTCTTCGGCCGCCGGCGCTACGTGCCCGACCTCAACGCCCGGGTGAAGAGCGTGCGGGAGGCGGCGGA

DNAPTAQ  ................C...........A.....AG.G.............................C..  2234
DNAPTFL  ......................T...................................C...........  2231
DNAPTTH  ..........AA.AA........................................CA.......C.....  2240

MAJORITY GCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGCCGACCTCATGAAGCTGGCCATGGTGAAGCTC

DNAPTAQ  .........................................................T............  2304
DNAPTFL  .....................G..........................................CG...T  2301
DNAPTTH  ......................................................C...............  2310

MAJORITY TTCCCCCGGCTXCAGGAAATGGGGGCCAGGATGCTCCTXCAGGTCCACGACGAGCTGGTCCTCGAGGCCC

DNAPTAQ  ......A....GG.........................T...............................  2374
DNAPTFL  ...........T......C.......G........TT.G.....G.........................  2371
DNAPTTH  ........C..C.G...G.........C.C........C.................CC....G.......  2380

MAJORITY CCAAAGAGCGGGCGGAGGXGGTGGCCGCTTTGGCCAAGGAGGTCATGGAGGGGGTCTATCCCCTGGCCGT

DNAPTAQ  .A......A.........CC......CGGC.........................G..............  2444
DNAPTFL  ....G..C.........AG...A..................................GG......CAG..  2441
DNAPTTH  ..C...C......C....A......G................C.......AA..C.........C.....  2450
```

FIG. 2G

2070908 .08T800T

```
MAJORITY GCCCCTGGAGGTGGAGGTGGGGATGGGGGAGGACTGGCTCTCCGCCAAGGAGTAG

DNAPTAQ  .....................A.........................GA   2499
DNAPTFL  ....................CC.............................   2496
DNAPTTH  ....................................T.........GT...   2505
```

FIG. 2H

```
MAJORITY MXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEPVQAVYGFAKSLLKALKEDG·DAVXVVFDAK

TAD PRO  .RG.....H.....·...I.....  69
TFL PRO  .·.....·.V.V.....  68
TTH PRO  .E.....YK..F.....  70

MAJORITY APSFRHEAYEAYKAGRAPTPEDFPROLALIKELVDLLGLXRLEVPGYEADDVLATLAKKAEKEGYEVRIL

TAG PRO  .....GG.....A.....S.....  139
TFL PRO  .....V.....F.....R.....  138
TTH PRO  .....FT.....  140

MAJORITY TADRDLYQLLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPSDNLPGVKGIGEKTAXKLLX

TAG PRO  ...K.....H.....D..A.....T..E.....R...E  209
TFL PRO  .....E...I.....Y.....A.....I.....QR.IR  208
TTH PRO  .....V...V.....H....E.....F...V.....L...K  210

MAJORITY EWGSLENLLKNLDRVKP·XXREKIXAHMEDLXLSXXLSXVRTDLPLEVDFAXRREPDREGLRAFLERLEF

TAG PRO  ......A.....L..·AI....L...D..K..WD.AK.....K.....R.....  278
TFL PRO  .....FQH..Q...·SL...LQ.G..A.A..RK..Q.H.....GR..T.NL.....  277
TTH PRO  .....ENV....K..L...R..LE..R.....L.QG.....  280

MAJORITY GSLLHEFGLLEXPKALEEAPWPPPEGAFVGFVLSRPEPMWAELLALAAARXGRVHRAXDPLXGLRDLKEV

TAG PRO  .....S.....K.....D.....PE.YKA.....A  348
TFL PRO  .....G...A.....L..SF.....G.WE..L...Q...R.....G.  347
TTH PRO  .....A.AP.....K....C.D.....A...A..K.....  350
```

FIG. 3A

```
MAJORITY RGLLAKDLAVLALREGLDLXPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEDAGERALLSERLFXNLXX

TAQ PRO  ........S........G.P................................E.....A......A..WG   418
TFL PRO  ..I................F.E......................................A....QT.KE   417
TTH PRO  ............S......V..................................AH........HR..LK   420

MAJORITY RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEIRRLEEEVFRLAGHPFNLNSRD

TAQ PRO  ............R...R...A.................R..........A...A................   488
TFL PRO  ..K.........E...........R....................EA.V.Q...................   487
TTH PRO  ......K.....H...............................L.........................   490

MAJORITY QLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKNTYIDPLPXLVHPRTG

TAQ PROO ......................................................S.......D.I.....   558
TFL PRO  .........................................DR...................A....K..   557
TTH PRO  ..........R...L...Q...........................H..........V....S.......   560

MAJORITY RLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFVAEEGWXLVALDYSQIELRVLAHLSGDENL

TAQ PRO  ........................................I.....L.......................   628
TFL PRO  ..............................................V..V....................   627
TTH PRO  ...........................................A..A.......................   630

MAJORITY IRVFQEGRDIHTQTASWMFGVPPEAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAVAFIERYFQ

TAQ PRO  ............E.........R......................................Q........   698
TFL PRO  .....................S..G..........................G..S...............   697
TTH PRO  .......K............................V.................................   700
```

FIG. 3B

20708090 "90818001

```
MAJORITY SFPKVRAWIEKTLEEGRRRGYVETLFGRRRYVPDLNARVKSVREAAERMAFNMPVQGTAADLMKLAMVKL

TAQ PRO  .....................................E.................................  768
TFL PRO  .Y........G.....................................................R.  767
TTH PRO  ................K.....................................................  770

MAJORITY FPRLXEMGARMLLQVHDELVLEAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX

TAQ PRO  ....E.................E...A..R.....................I.........  833
TFL PRO  ....Q.L...............D...R............W..Q........L.........  831
TFL PRO  ....R.............L....QA...E.......A..KA............M........G  835
```

FIG. 3C

Genes for Wild-Type and Pol(–)DNAPTaq

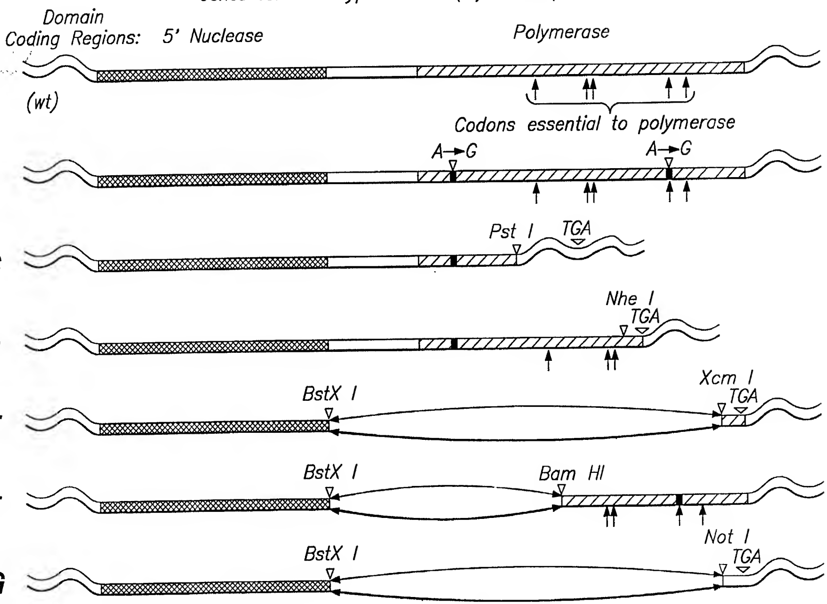


FIG. 4A

FIG. 4B

FIG. 4C

FIG. 4D

FIG. 4E

FIG. 4F

FIG. 4G

20/090' 90ST80QT

Genes for Wild-Type and Pol(–)DNAPTfl

FIG. 5A

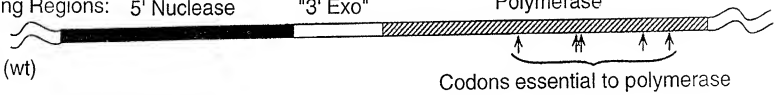
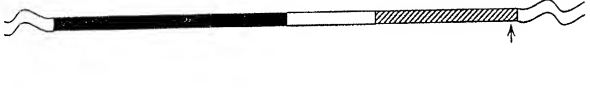


FIG. 5B



10031806.060702

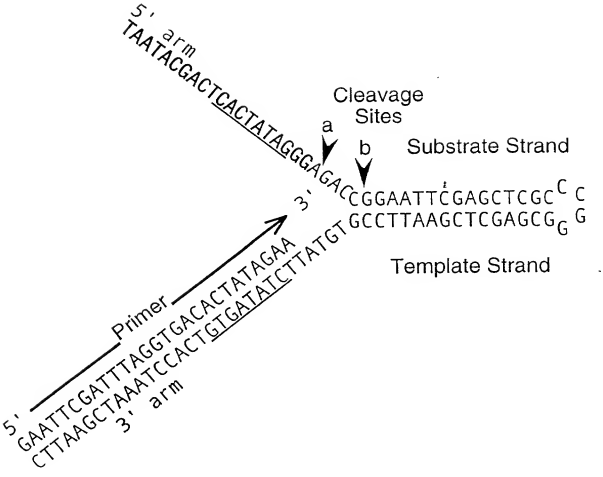


FIG. 6

10081805.050702

FIG. 7

10081306.060702

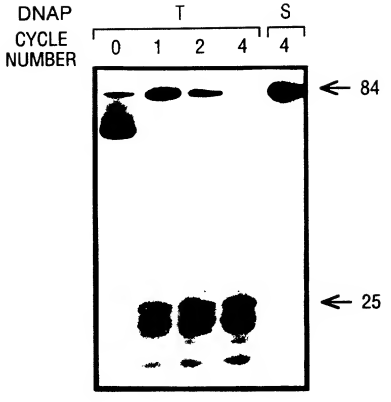


FIG. 8

10081805.060702

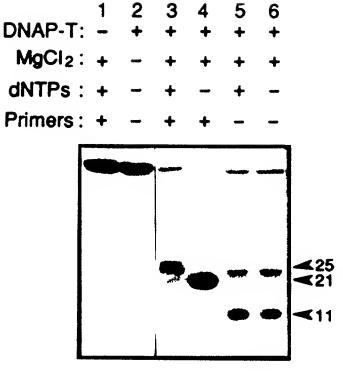


FIG. 9A

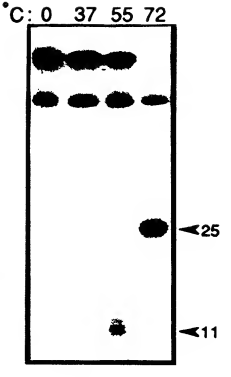


FIG. 9B

20070902.0608180

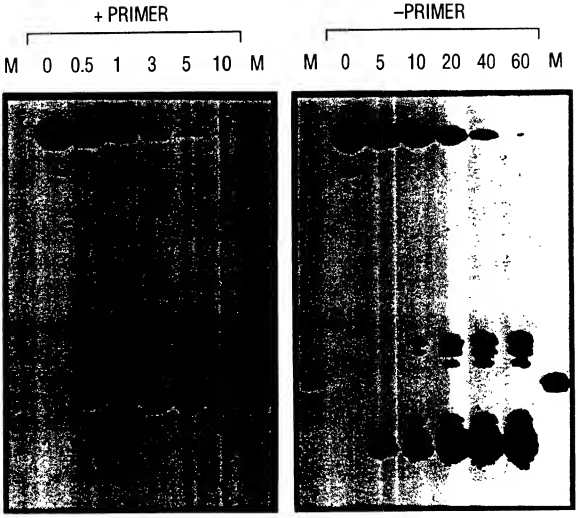


FIG. 10A

FIG. 10B

20070905.0807008

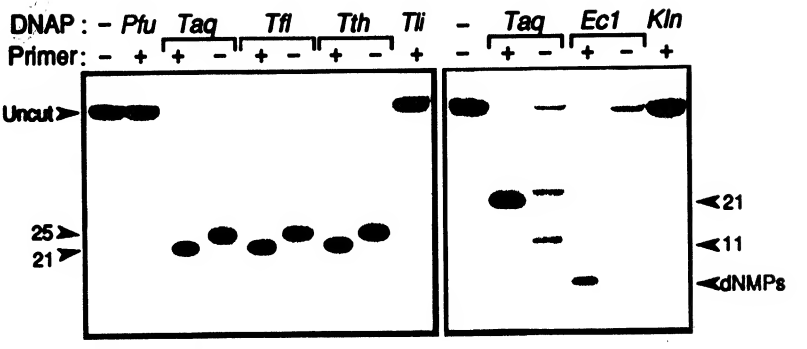


FIG. 11A

FIG. 11B

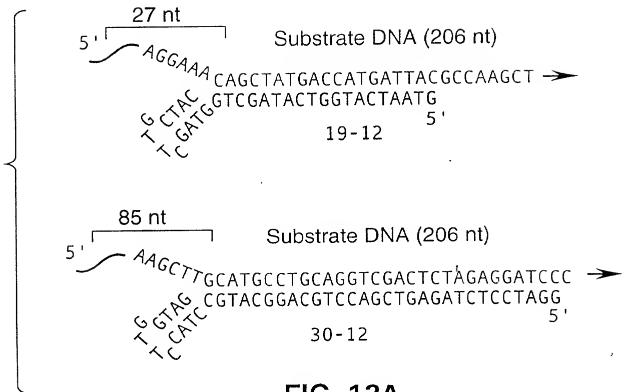


FIG. 12A

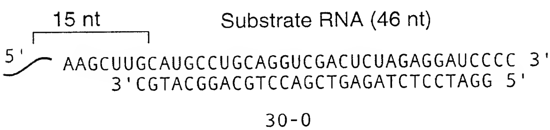


FIG. 13A

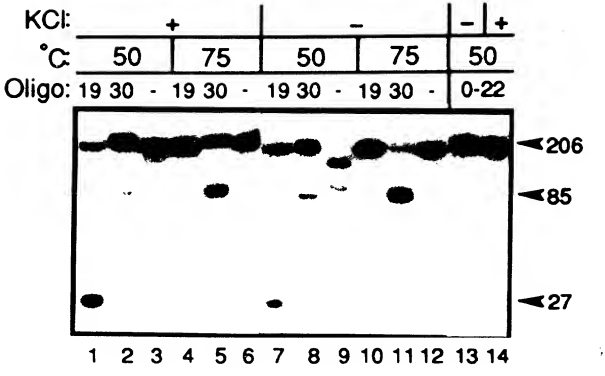


FIG. 12B

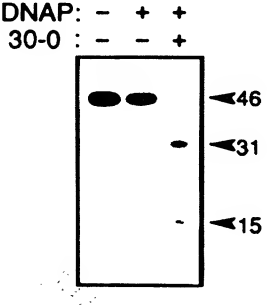
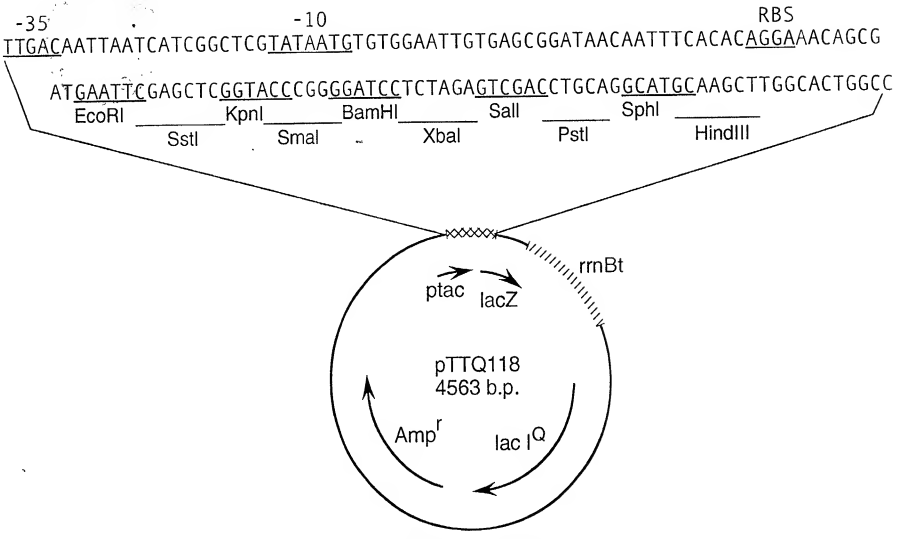


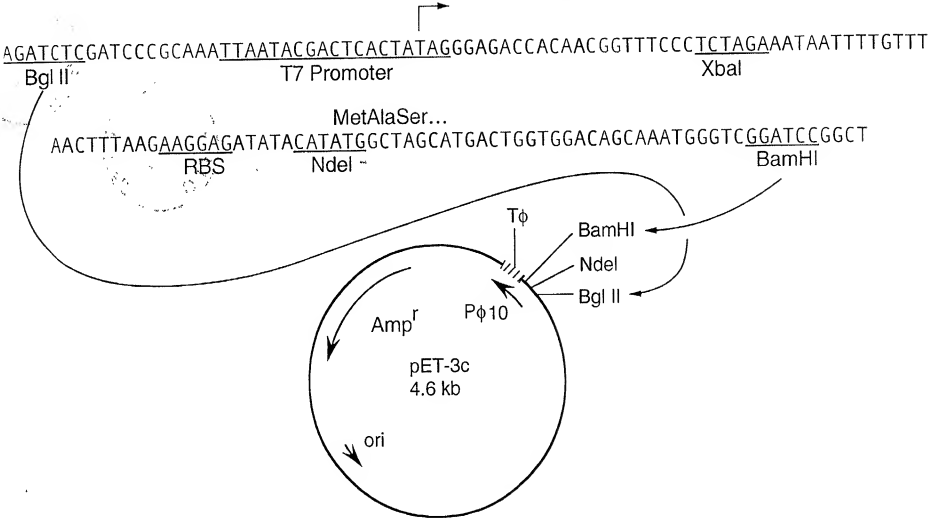
FIG. 13B

10081805.060702



RBS: Ribosome binding site
ptac: Synthetic tac promoter
lac I^Q: Lac repressor gene
lacZ: Beta-galactosidase alpha fragment
rrnBt: E. coli rrnB transcription terminator

FIG. 14



$P_{\phi 10}$: Bacteriophage T7 ϕ10 promoter RBS: Ribosome binding site
Tϕ: T7 ϕ Terminator

FIG. 15

20070902 1008186

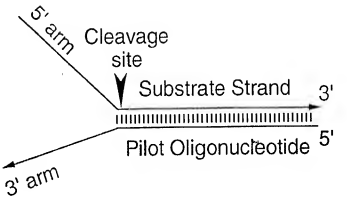


FIG. 16A

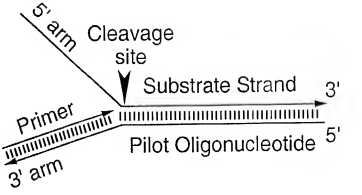


FIG. 16B

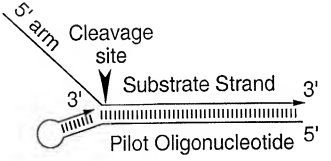


FIG. 16C

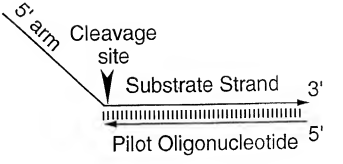


FIG. 16D

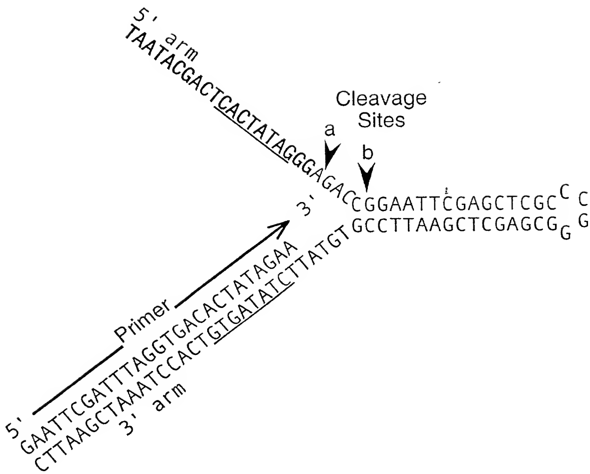

5' arm
TAATACGACTCACTATAGGGAGAC
Cleavage Sites
a
b
CGGAATTCGAGCTCGC C C
3'
GCCTTAAGCTCGAGCG G G
Primer
5'
GAATTCGATTTAGGTGACACTATAGAA
CTTAAGCTAAATCCACTGTGATATCTTATGT
3' arm

FIG. 16E

2070901 90818001

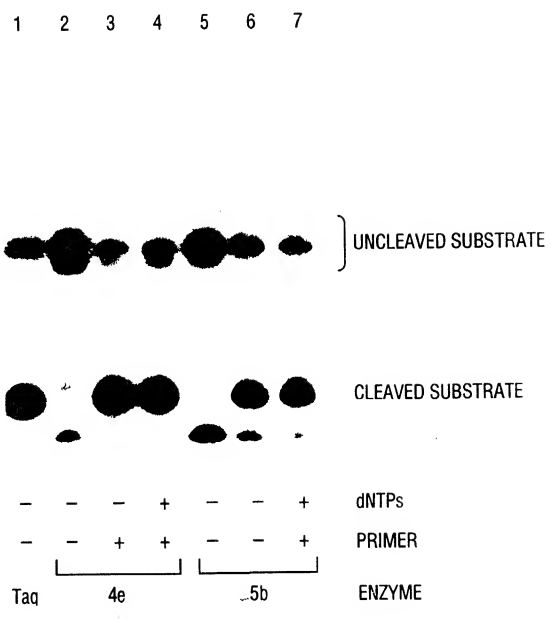


FIG. 17

20709D 90818001

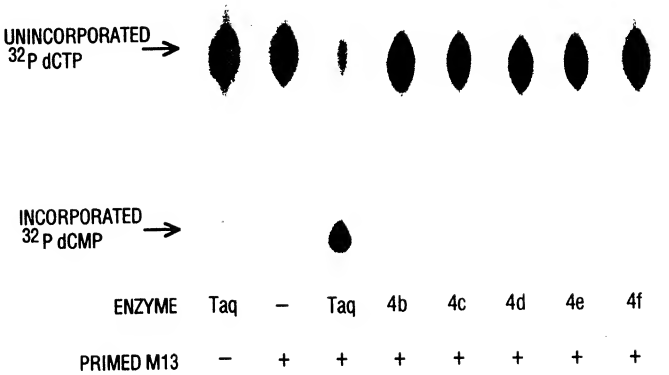


FIG. 18

10021806.060702

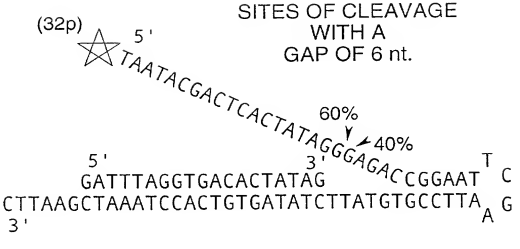


FIG. 19A

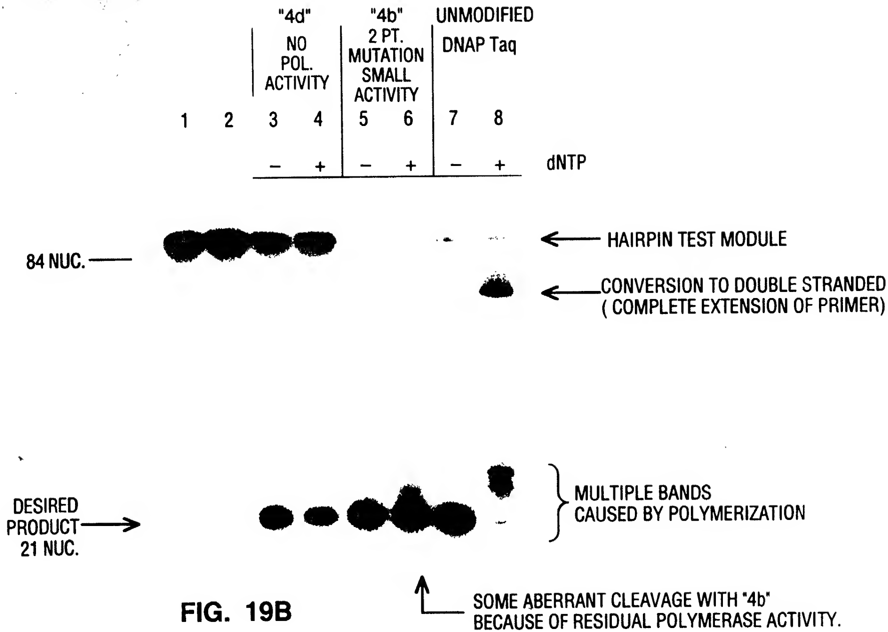

"4d"
NO
POL.
ACTIVITY
"4b"
2 PT.
MUTATION
SMALL
ACTIVITY
UNMODIFIED
DNAP Taq
1 2 3 4 5 6 7 8
− + − + − +
dNTP
84 NUC.
HAIRPIN TEST MODULE
CONVERSION TO DOUBLE STRANDED
(COMPLETE EXTENSION OF PRIMER)
DESIRED
PRODUCT
21 NUC.
MULTIPLE BANDS
CAUSED BY POLYMERIZATION
SOME ABERRANT CLEAVAGE WITH "4b"
BECAUSE OF RESIDUAL POLYMERASE ACTIVITY.

FIG. 19B

20Z090'90ST800T

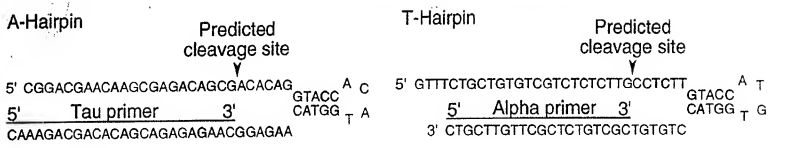


FIG. 20A

Sequence of alpha primer:
5' GACGAACAAGCGAGACAGCG 3'

FIG. 20B

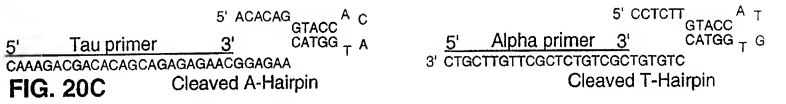


FIG. 20C

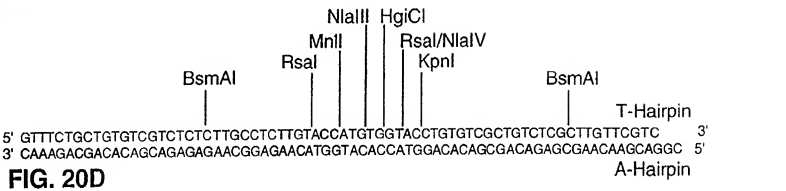


FIG. 20D

20070902 10081806

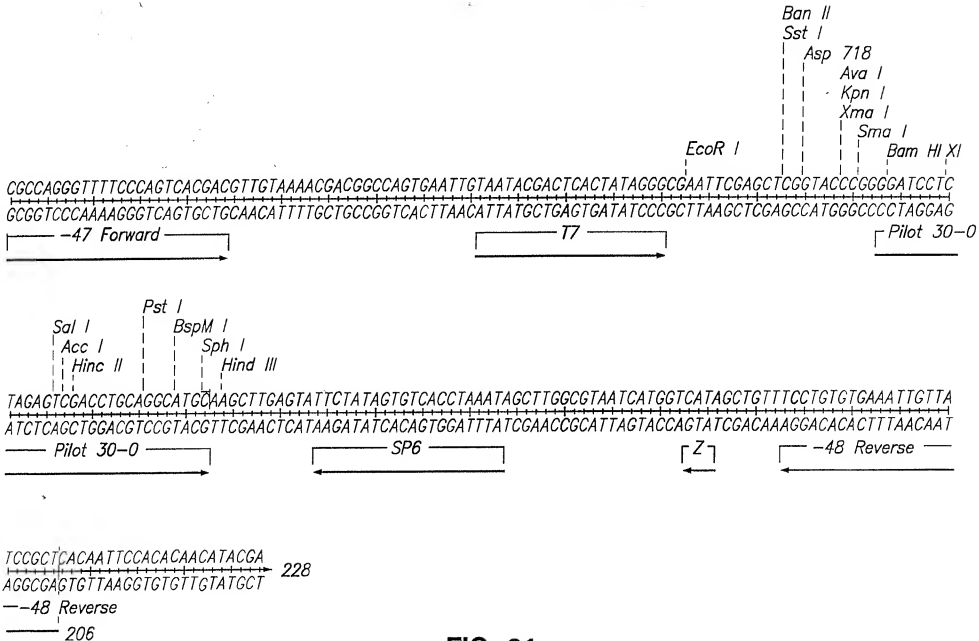


FIG. 21

10081806.060702

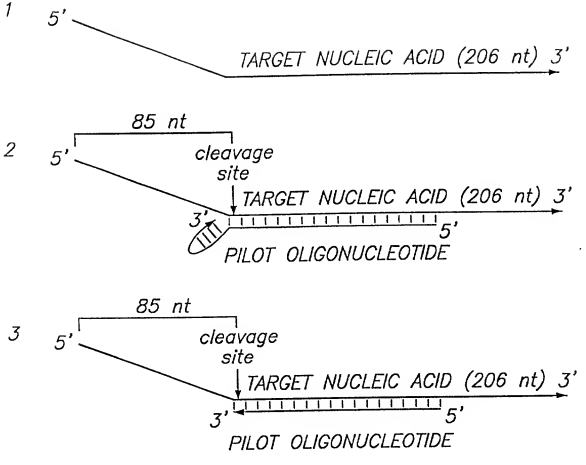


FIG. 22A

20/090 .90818001

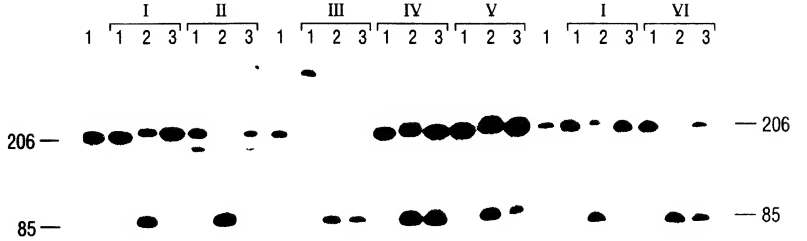


FIG. 22B

20070902 .0818006

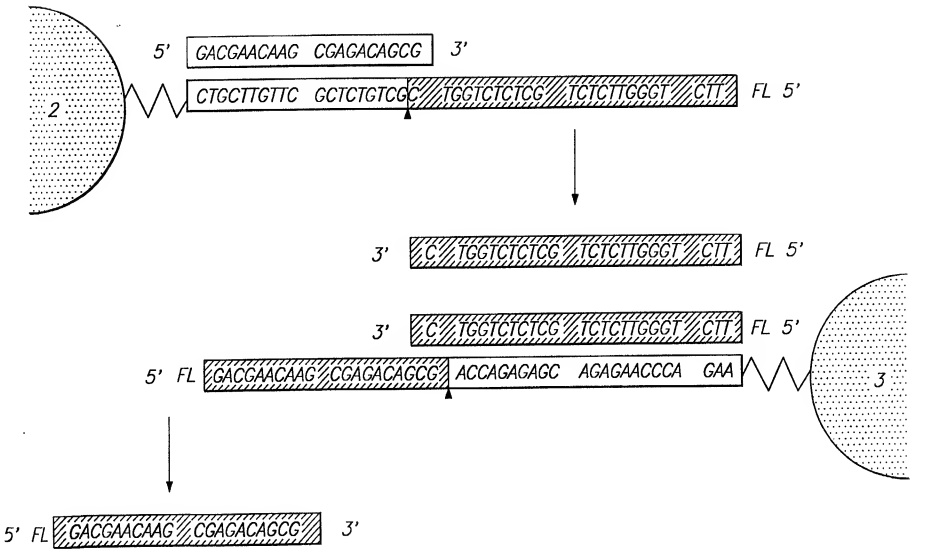


FIG. 23

20070602.0082806

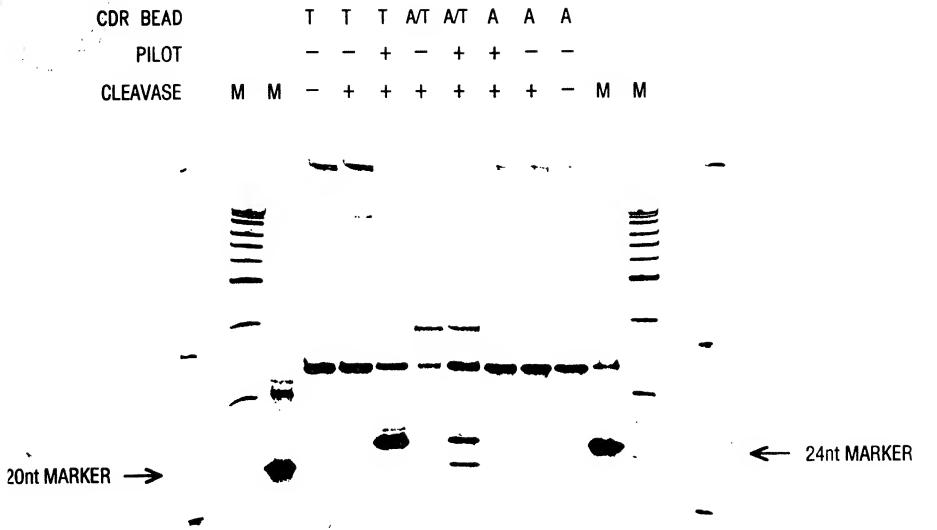


FIG. 24

20708090 .90818001

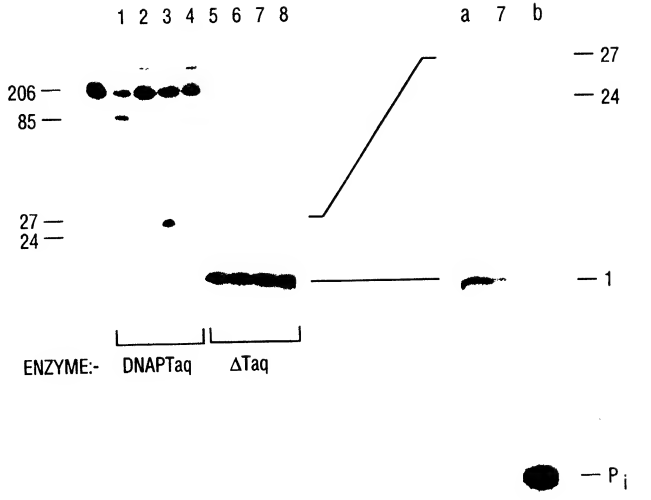


FIG. 25A

FIG. 25B

20070902.1009180

FIG. 26A

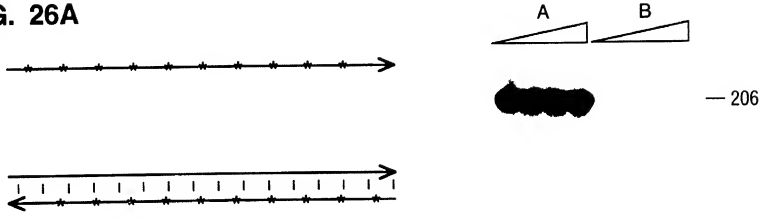


FIG. 26B

* = ^{32}P

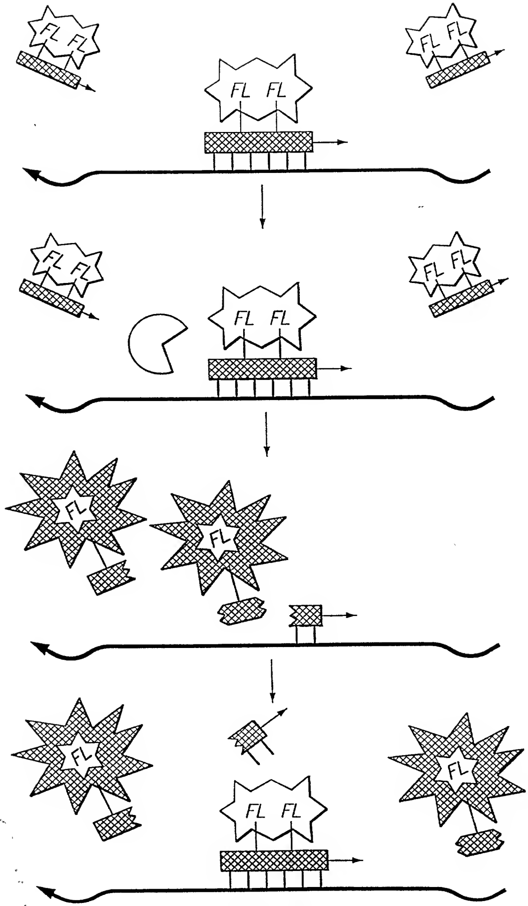


FIG. 27

10081805.060702

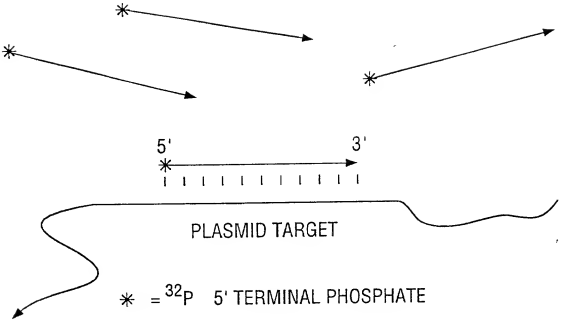


FIG. 28A

10081805.060702

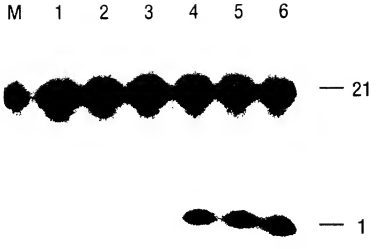


FIG. 28B

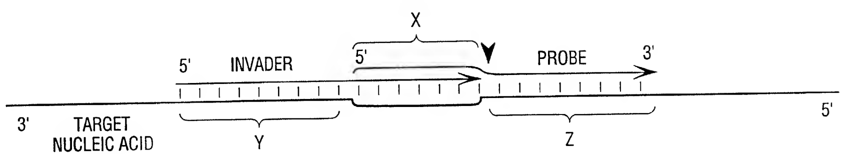


FIG. 29

1008180 .060702

FIG. 30

10081806.060702

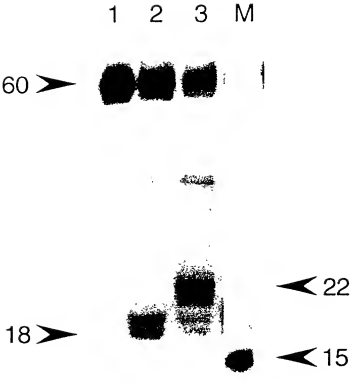


FIG. 31

20/090,908

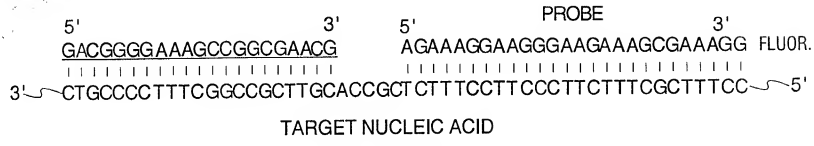


FIG. 32A

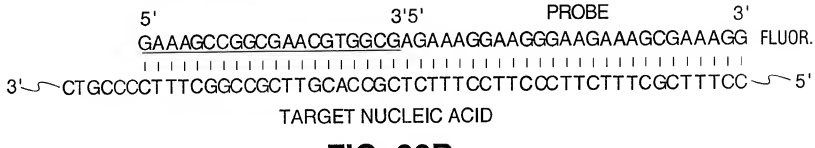


FIG. 32B

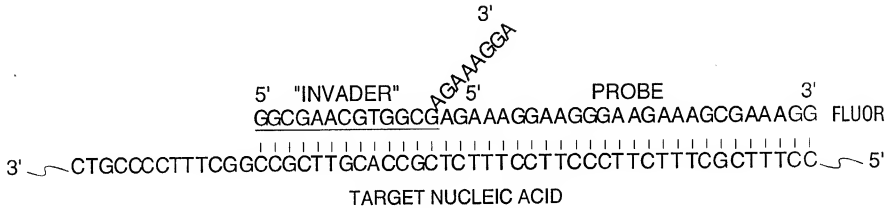


FIG. 32C

20070902 .0081806

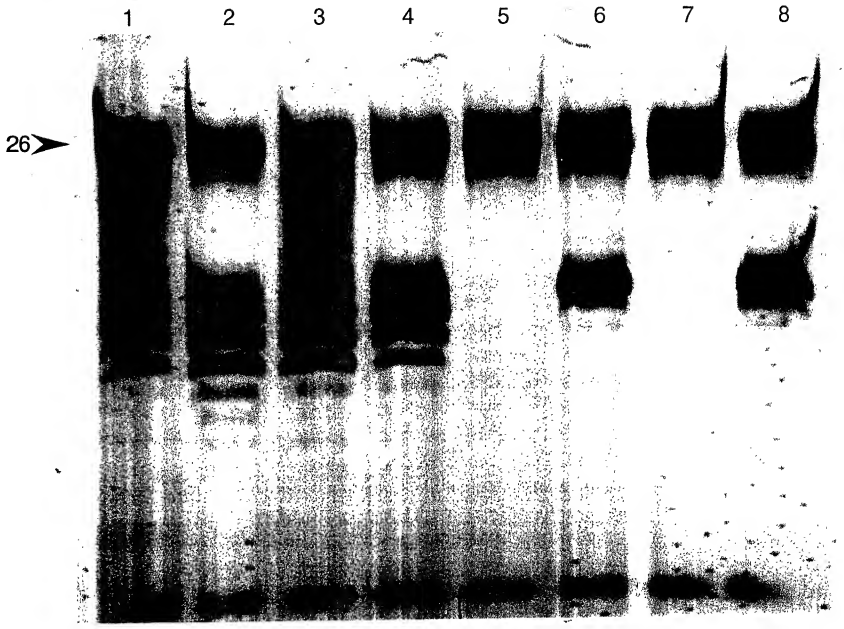


FIG. 33

20070902.0908180021

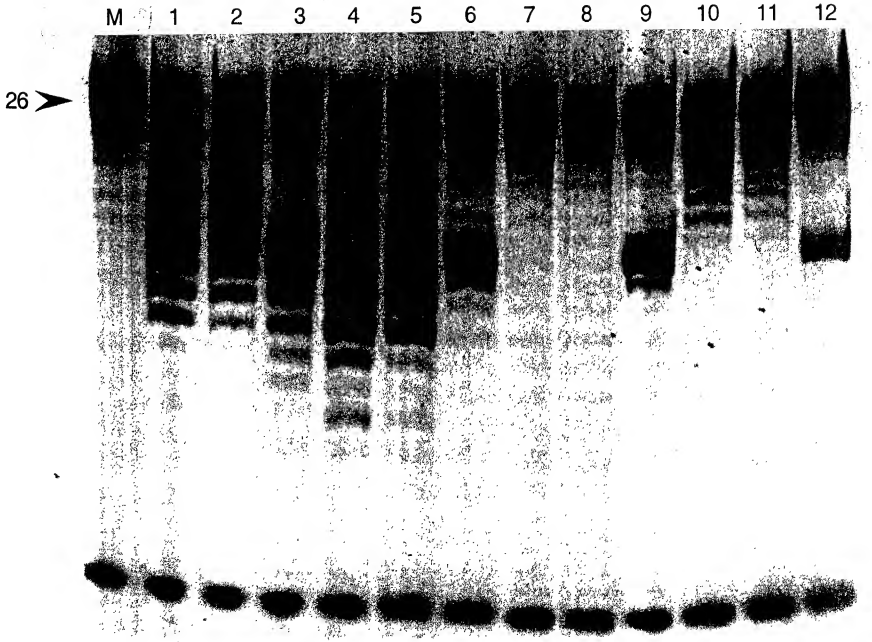


FIG. 34

10081805.060702

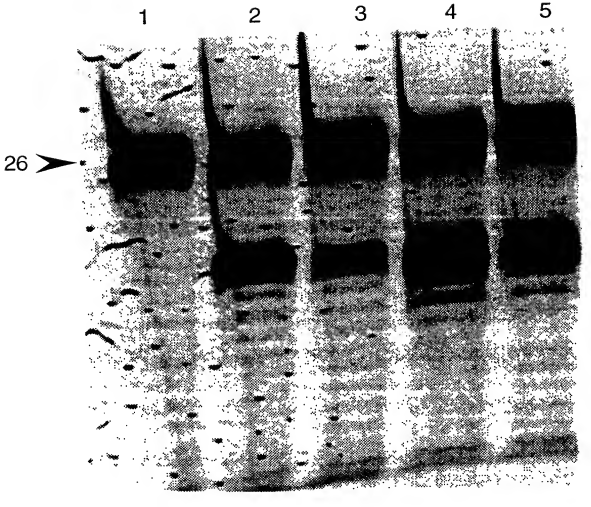


FIG. 35

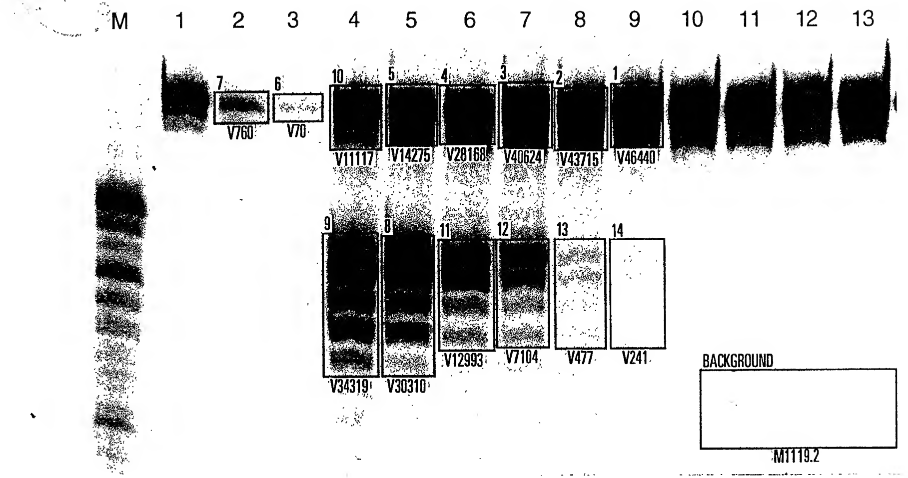

M
1
2
3
4
5
6
7
8
9
10
11
12
13
7 V760
6 V70
10 V11117
5 V14275
4 V28168
3 V40624
2 V43715
1 V46440
9 V34319
8 V30310
11 V12993
12 V7104
13 V477
14 V241
BACKGROUND
M1119.2

FIG. 36

20070902.0081806

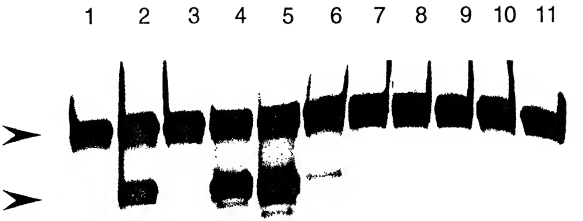


FIG. 37

20070902.1008806

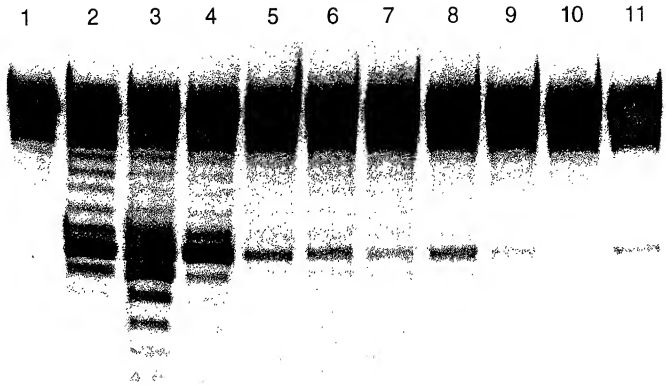


FIG. 38

10081805.060702

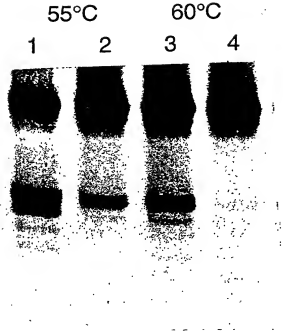


FIG. 39

10061805.060702

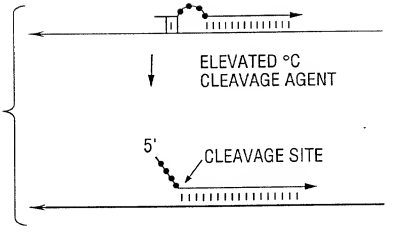


FIG. 40A

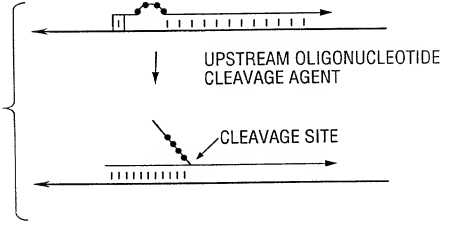


FIG. 40B

20070902 10081806

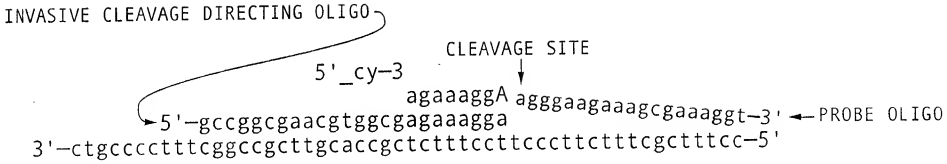


FIG. 41

10081605.060702

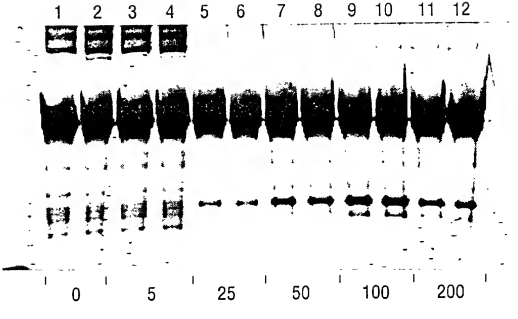


FIG. 42

10081806-060702

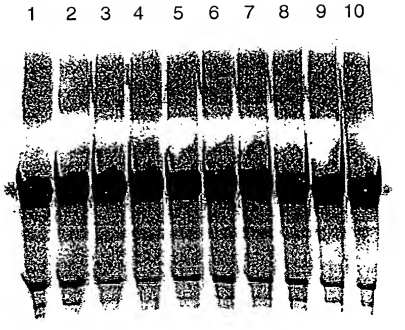


FIG. 43

20020306-000302

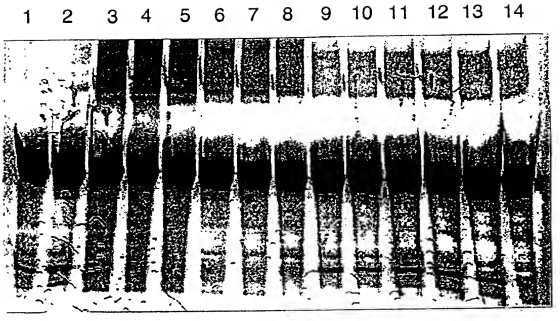


FIG. 44

20090'30818001

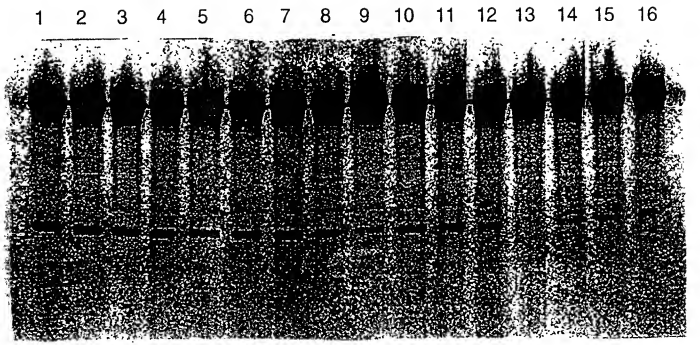


FIG. 45

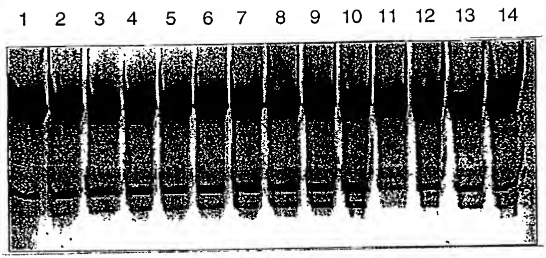


FIG. 46

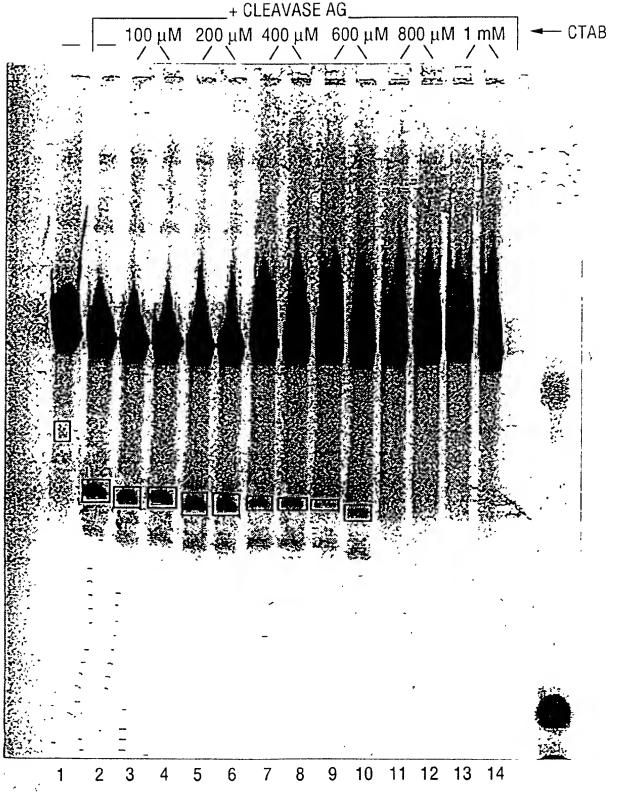


FIG. 47

10081606.060702

10081805.060702

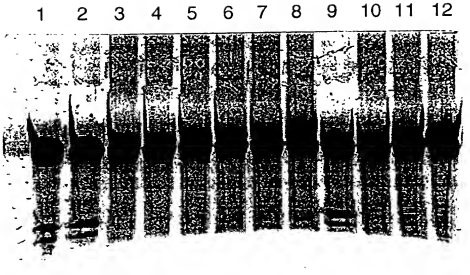


FIG. 48

10031806.050702

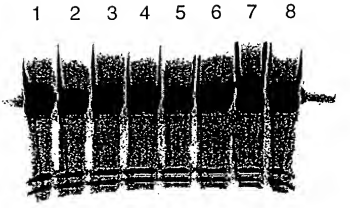


FIG. 49

10081206.060702

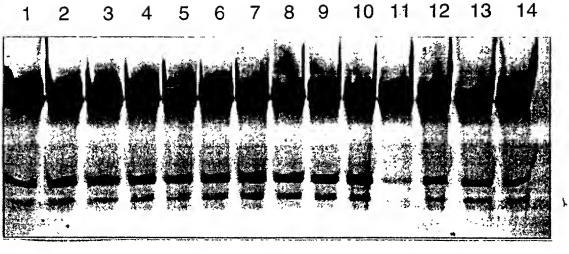


FIG. 50

10081806.060702

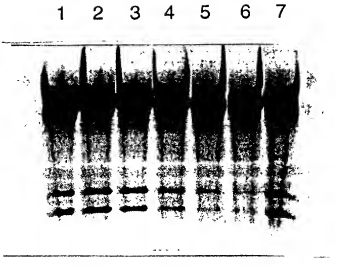


FIG. 51

10061805.060702

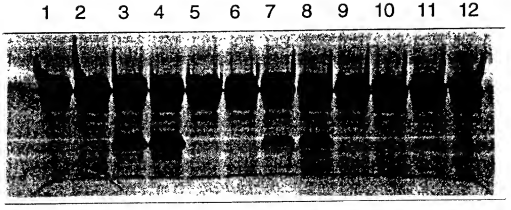


FIG. 52

20070902.0081806

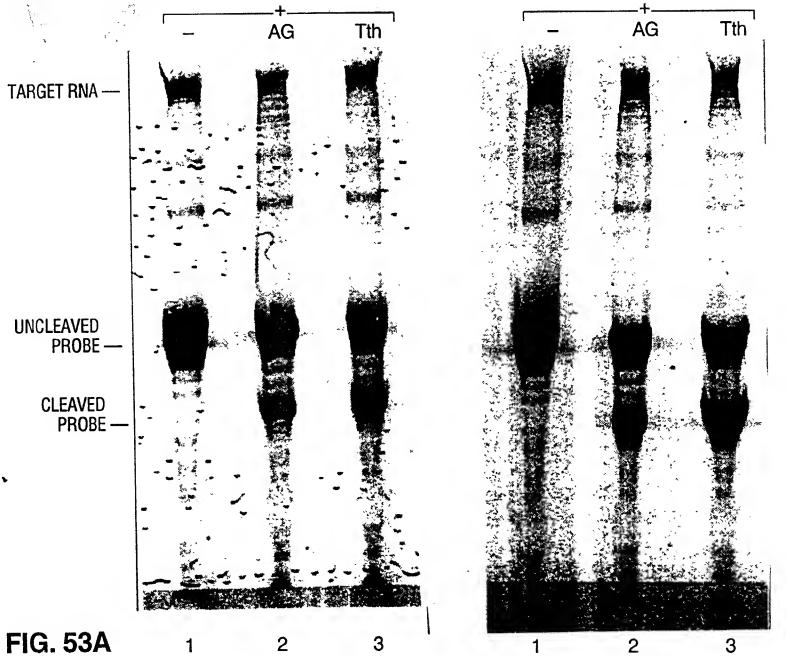


FIG. 53A

FIG. 53B

20070902.0082506

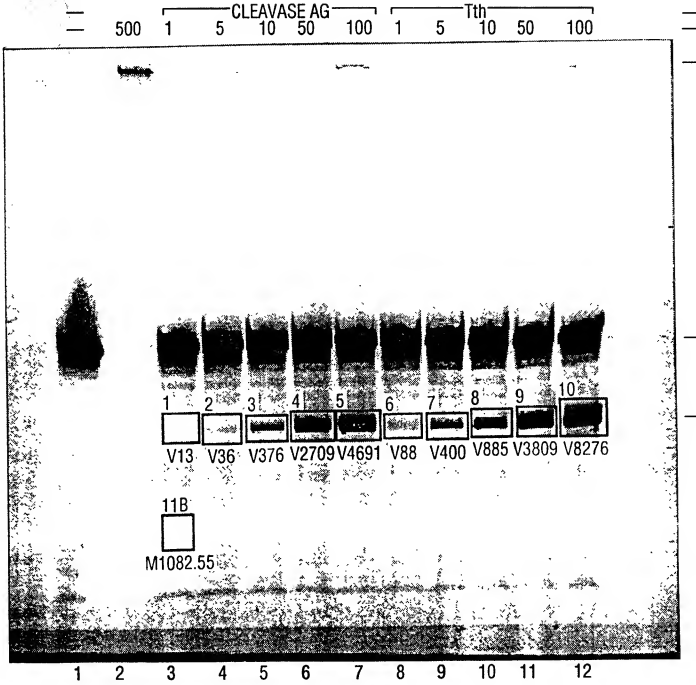


FIG. 54

10061806-060702

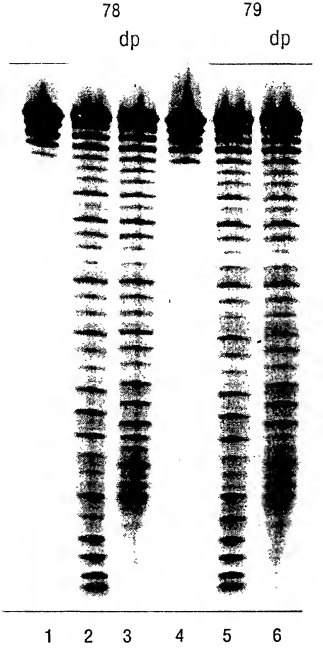


FIG. 55

70 (C10 amino T's)
74 (C6 amino T's)

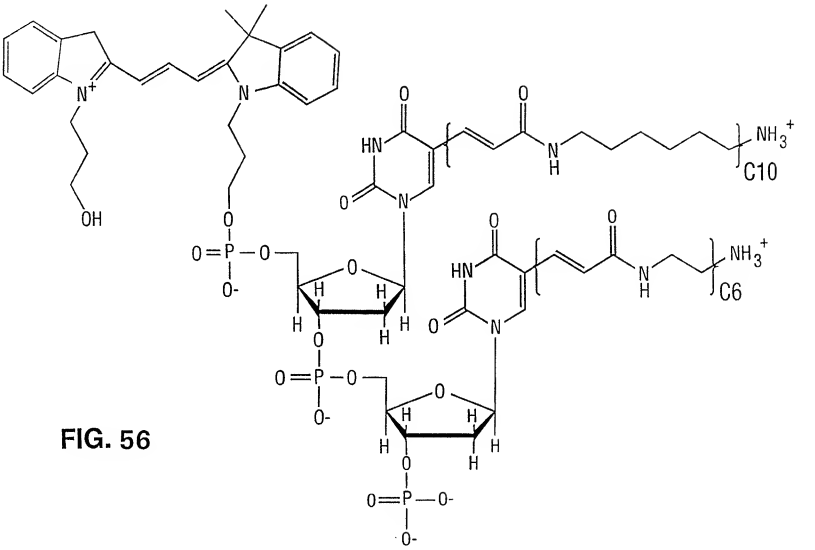


FIG. 56

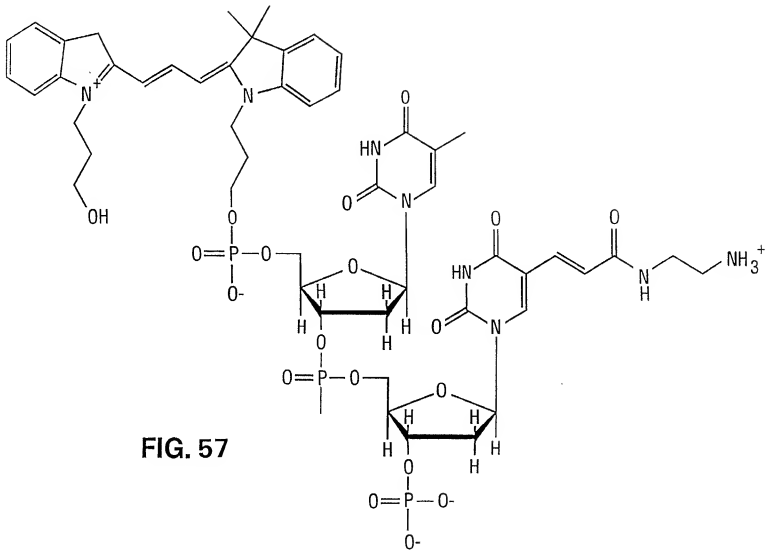


FIG. 57

76

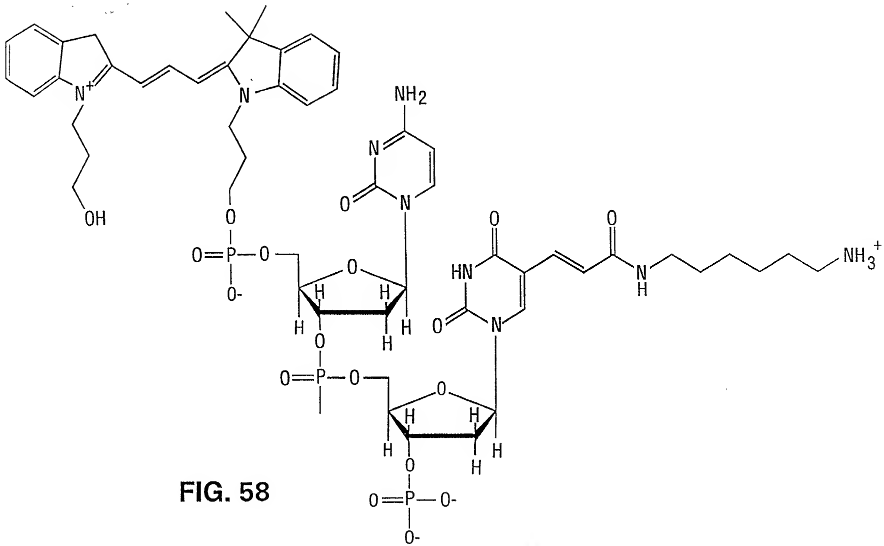


FIG. 58

10081805.060702

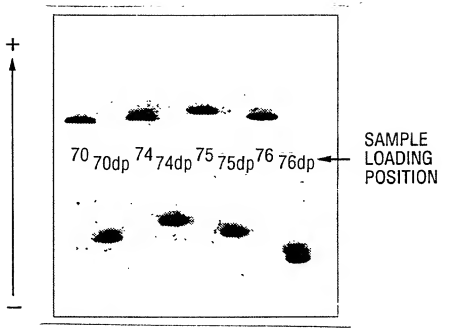


FIG. 59

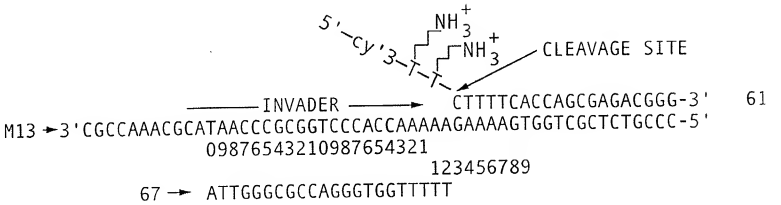

5'-Cy3-
NH3+
NH3+
CLEAVAGE SITE
INVADER
CTTTTCACCAGCGAGACGGG-3'
61
M13 3'CGCCAAACGCATAACCCGCGGTCCCACCAAAAAGAAAAGTGGTCGCTCTGCCC-5'
09876543210987654321
123456789
67 ATTGGGCGCCAGGGTGGTTTTT

FIG. 60A

10031806.060702

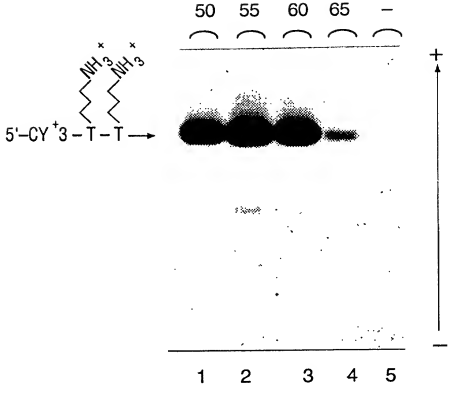


FIG. 60B

1006180S.050702

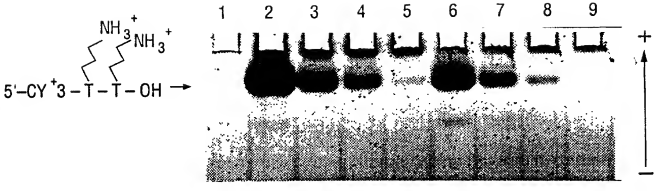


FIG. 61

10081805.060702

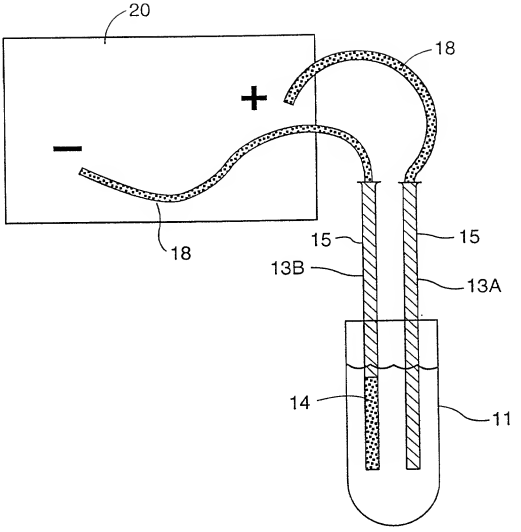


FIG. 62

20070702.9081806

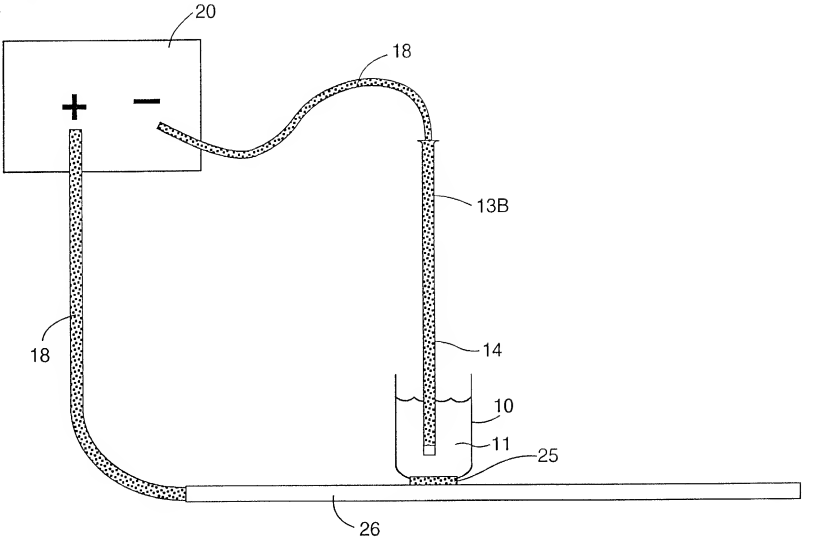


FIG. 63

10081805.060702

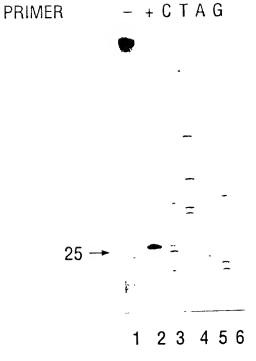


FIG. 64

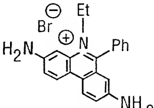
FIG. 65A

FIG. 65B

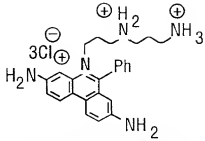
FIG. 65C

FIG. 65D

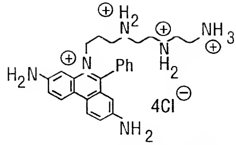
20070202.0850081



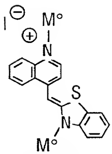
ETHIDIUM BROMIDE



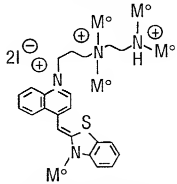
(1,3-PROPANEDIAMINO)-PROPIDIUM



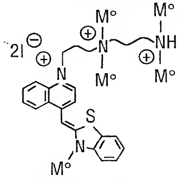
(DIETHYLENETRIAMINO)-PROPIDIUM



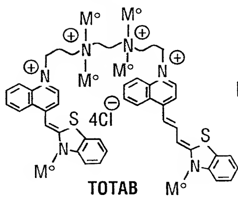
THIAZOLE ORANGE



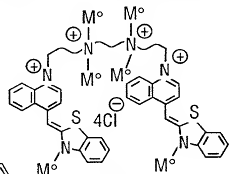
(N-N'-TETRAMETHYL-1,2-ETHANEDIAMINO)-PROPYL THIAZOLE ORANGE



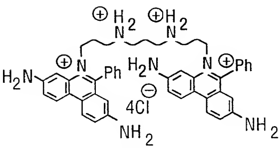
(N-N'-TETRAMETHYL-1,3-PROPANEDIAMINO)-PROPYL THIAZOLE ORANGE



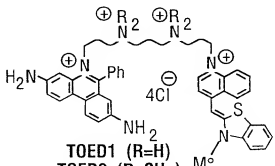
TOTAB



TOTO

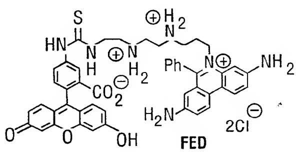


EthD



TOED1 (R=H)
TOED2 (R=CH_3)

FIG. 66



FED

10081806.050702

20070907.0607202

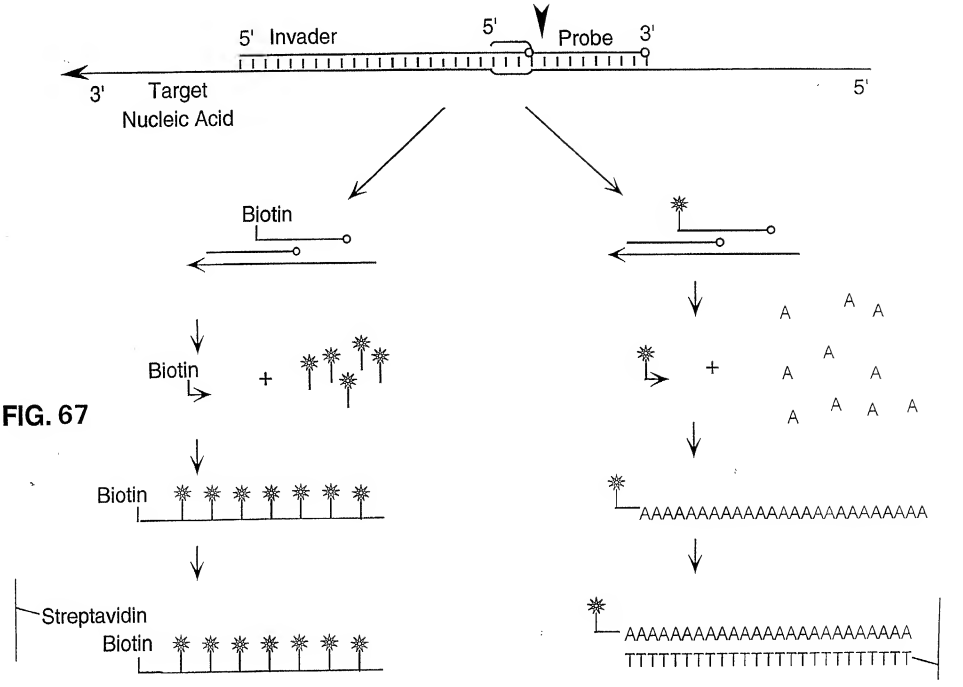


FIG. 67

10081606.060702

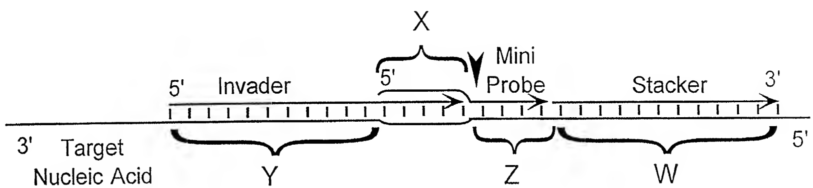


FIG. 68

10021805.050702

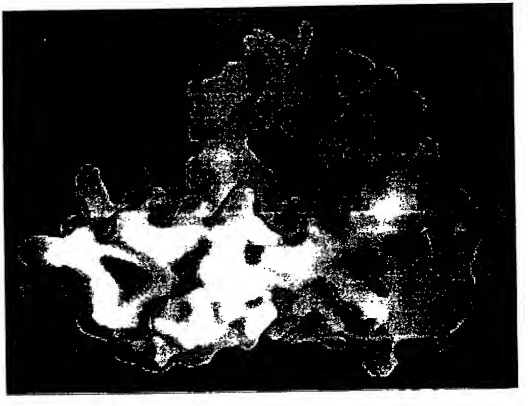


FIG. 69

```
            10        20        30        40        50        60        70
1  MGVQ-----FGDFIPK--NIISFEDLKGKKVAIDGMNALYQFLTSIRLRDGSPLRNRKGEITSAYNGVFY MJAFEN1.PRO
1  MGVP-----IGEIIPR--KEIELENLYGKKIAIDALNAIYQFLSTIRQKDGTPLMDSKGRITSHLSGLFY PFUFEN1.PRO
1  MGIQGLAKLIADVAPSAIRENDIKSYFGRKVAIDASMSIYQFLIAVRQ-GGDVLQNEEGETTSHLMGMFY HUMFEN1.PRO
1  MGIHGLAKLIADVAPSAIRENDIKSYFGRKVAIDASMSIYQFLIAVRQ-GGDVLQNEEGETTS-LMGMFY MUSFEN1.PRO
1  MGIKGLNAIISEHVPSAIRKSDIKSFFGRKVAIDASMSLYQFLIAVRQQDGGQLTNEAGETTSHLMGMFY YST510.PRO
1  MGVHSFWDIAG----PTARPVRLESLEDKRMAVDASIWIYQFLKAVRDQEGNAVKN------SHITGFFR YSTRAD2.PRO
1  MGVSGLWNILE----PVKRPVKLETLVNKRLAIDASIWIYQFLKAVRDKEGNQLKS------SHVVGFFR SPORAD13.PRO
1  MGVQGLWKLLE----CSGROVSPEALEGKILAVDISIWLNQALKGVRDRHGNSIEN------PHLLTLFH HUMXPG.PRO
1  MGVQGLWKLLE----CSGHRVSPEALEGKVLAVDISIWLNQALKGVRDSHGNVIEN------AHLLTLFH MUSXPG.PRO
1  MGVQGLWKLLE----CSGRPINPGTLEGKILAVDISIWLNQAVKGARDRQGNAIQN------AHLLTLFH XENXPG.PRO
1  MTINGIWEWANHVV----RKVPNETMRDKTLSIDGHIWLYESLKGCEAHHQQT-------PNSYLVTFFT CELRAD2.PRO

            80        90       100       110       120       130       140
64 KTIHLLENDITPIWVFDGEPPKLKEKTRKVRREMKEKAELKMKEAIKK----EDFEEAAKYAKRVSYLTP MJAFEN1.PRO
64 RTINLMEAGIKPVYVFDGEPPEFKKKELEKRREAREEAEEKWREALEK----GEIEEARKYAQRATRVNE PFUFEN1.PRO
70 RTIRMMENGIKPVYVFDGKPPQLKSGELAKRSERRAEAEKQLQQAQAA----GAEOEVEKFTKRLVKVTK HUMFEN1.PRO
69 RTIRM-ENGIKPVYVFDGKPPQLKSGELAKRSERRAEAEKQLQQAQEA----GMEEEVEKFTKRLVKVTK MUSFEN1.PRO
71 RTLRMIDNGIKPCYVFDGKPPDLKSHELTKRSSRRVETEKKLA---EA----TTELEKMKQERRLVKVSK YST510.PRO
61 RICKLLYFGIRPVFVFDGGVPVLKRETIRQRKERRQGKRESAKSTARKLLALQLQNGSNDNKRDSDEVTM YSTRAD2.PRO
61 RICKLLFFGIKPVFVFDGGAPSLKRQTIQKRQARRLDREENATVTANKLLALQMRHQAMLLKRDADEVTQ SPORAD13.PRO
61 RLCKLLFFRIRPIFVFDGDAPLLKKQTLVKRRQRKDLASSDSRKTTEKLLKTFLKRQAIKTERIAATVTG HUMXPG.PRO
61 RLCKLLFFRIRPIFVFDGDAPLLKKQTLAKRRQRKDSASIDSRKTTEKLLKTFLKRQALKTDRIAASVTG MUSXPG.PRO
61 RLCKLLFFRIRPIFVFDGEAPLLKRQTLAKRRQRTDKASNDARKTNEKLLRTFLKRQAIKAERIAATVTG XENXPG.PRO
60 RIQRLLELKIIPIVVFDNINASSSAHESKDQNEFVPRKRRSFGDSPFTNLV------------------- CELRAD2.PRO
```

FIG. 70A

20/090"908T800T

```
         150       160       170       180       190       200       210
130 KMVENCKYLLSLMGIPYVEAPSEGEAQASYMAKKGDVWAVVSQDYDALLYGAPRVVRNLTTTKEM------ MJAFEN1.PRO
130 MLIEDAKKLLELMGIPIVQAPSEGEAQAAYMAAKGSVYASASQDYDSLLFGAPRLVRNLTITGKRKLPGK PFUFEN1.PRO
136 QHNDECKHLLSLMGIPYLDAPSEAEASCAALVKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIQ HUMFEN1.PRO
134 QHNDECKHLLSLMGIPYLDAPSEAEASCAALAKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIQ MUSFEN1.PRO
134 EHNEEAQKLLGLMGIPYIIAPTEAEAQCAELAKKGKVYAAASEDMDTLCYRTPFLLRHLTFSEAKKEPIH YST510.PRO
131 DMIKEVQELLSRFGIPYITAPMEAEAQCAELLQLNLVDGIITDDSDVFLFGGTKIYKNMFHEKNY---VE YSTRAD2.PRO
131 VMIKECQELLRLFGLPYIVAPOEAEAQCSKLLELKLVDGIVTDDSDVFLFGGTRVYRNMFNQNKF---VE SPORAD13.PRO
131 QMFLESQELLRLFGIPYIQAPMEAEAQCAILDLTDQTSGTITDDSDIWLFGARHVYRNFFNKNKF---VE HUMXPG.PRO
131 QMFLESQELLRLFGVPYIQAPMEAEAOCAVLDLSDQTSGTITDDSDIWLFGARHVYKNFFNKNKF---VE MUSXPG.PRO
131 QMCLESQELLQLFGIPYIVAPMEAEAQCAILDLTDQTSGTITDDSDIWLFGARHVYKNFFSQNKH---VE XENXPG.PRO
111 DHVYKTNALLTELGIKVIIAPGDGEAQCARLEQLGVTSGCITTDFDYFLFGGKNLYRFDFTAGT------ CELRAD2.PRO

         220       230       240       250       260       270       280
195 --------PELIELNEVLEDLRISLDDLIDIAIFMGTDYNPGGV--K--GIGFKRAYELVRSGVAK--DV MJAFEN1.PRO
200 NVYVE-IKPELIILEEVLKELKLTREKLIELAILVGTDYNPGGI--K--GIGLKKALEIVRHSKDPLAKF PFUFEN1.PRO
206 EFHLSRILQELGLNQEQFVDLCILLGSDYCESIRGIGPKRAVDLIQK--HKSIEEIVRRLDPN-----KY HUMFEN1.PRO
204 EFHLSRVLQELGLNQEQFVDLCILLGSDYCESIRGIGAKRAVDLIQK--HKSIEEIVRRLDPS-----KY MUSFEN1.PRO
204 EIDTELVLRGLDLTIEQFVDLCIMLGCDYCESIRGVGPVTALKLIKT--HGSIEKIVEFIESGESNNTKW YST510.PRO
198 FYDAESILKLLGLDRKNMIELAQLLGSDYTNGLKGMGPVSSIEVIAEF---GNLKNFKDWYNNGOFDKRK YSTRAD2.PRO
198 LYLMDDMKREFNVNQMDLIKLAHLLGSDYTMGLSRVGPVLALEILHEFPGDTGLFEFKKWFQRLSTGHAS SPORAD13.PRO
198 YYQYVDFHNQLGLDRNKLINLAYLLGSDYTEGIPTVGCVTAMEILNEFPGHGLEPLLKFSEWWHEAQKNP HUMXPG.PRO
119 YYQYVDFYSQLGLDRNKLINLAYLLGSDYTEGIPTVGCVTAMEILNEFPGRGLDPLLKFSEWWHEAQNNK MUSXPG.PRO
198 YYQYADIHNOLGLDRSKLINLAYLLGSDYTEGIPTVGYVSAMEILNEFPGQGLEPLVKFKEWWSEAQKDK XENXPG.PRO
175 ----------------------------------SSTACLHDIMHLSLGRMFM------------ CELRAD2.PRO
```

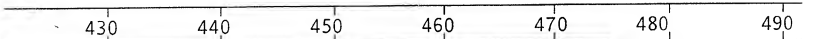
FIG. 70B

10081506.060702

```
                   290       300       310       320       330       340       350
251 LKKEVEYYDEIKRIFKEPKV-------------------TD--NYSLSLKLPDKEGIIKFLVDENDFNYD MJAFEN1.PRO
265 QKQSDVDLYAIKEFFLNPPV-------------------TD--NYNLVWRDPDEEGILKFLCDEHDFSEE PFUFEN1.PRO
269 PVPENWLHKEAHQLFLEPEV-------------------LDPESVELKWSEPNEEELIKFMCGEKQFSEE HUMFEN1.PRO
267 PVPENWLHKEAQQLFLEPEV-------------------VDPESVELKWSEPNEEELVKFMCGEKQFSEE MUSFEN1.PRO
272 KIPEDWPYKQARMLFLDPEV-------------------IDGNEINLKWSPPKEKELIEYLCDDKKFSEE YST510.PRO
265 QETENKFEKDLRKKLVNNEIILDDDFPSVMVYDAYMRPEVDHDTTPFVWGVPDLDMLRSFMKTQLGWPHE YSTRAD2.PRO
268 KNDVNTPVKKRINKLVGK-IILPSEFPNPLVDEAYLHPAVDDSKQSFQWGIPDLDELRQFLMATVGWSKQ SPORAD13.PRO
268 KIRPNPHDTKVKKKL--RTLQLTPGFPNPAVAEAYLKPVVDDSKGSFLWGKPDLDKIREFCQRYFGWNRT HUMXPG.PRO
268 KVAENPYDTKVKKKL--RKLQLTPGFPNPAVADAYLRPVVDDSRGSFLWGKPDVDKIREFCORYFGWNRM MUSXPG.PRO
268 KMRPNPNDTKVKKKL--RLLDLQQSFPNPAVASAYLKPVVDESKSAFSWGRPDLEQIREFCESRFGWYRL XENXPG.PRO
194 ------EKKVSRPHLISTAILLGCDYFORGVQNIGIVSVFD-ILGEFGDDGNEEIDPHVILDRFASYVRE CELRAD2.PRO

                   360       370       380       390       400       410       420
300 RVKKHVDKLYNLIA-------------------------------------------------------- MJAFEN1.PRO
314 RVKNGLERLKKAI--------------------------------------------------------- PFUFEN1.PRO
320 RIRSGVKRLSKSRQGS-TQGRLDDFFKVT----------------------------------------- HUMFEN1.PRO
318 RIRSGVKRLSKSRQGS-TQGRLDDFFKVT----------------------------------------- MUSFEN1.PRO
323 RVKSGISRLKKGLKSG-IQGRLDGFFOVV----------------------------------------- YST510.PRO
335 KSDEILIPLIRDVNKRKK------------------------------------------------KGKQ YSTRAD2.PRO
337 RTNEVLLPVIQDMHKKOF------------------------------------------------VGTQ SPORAD13.PRO
336 KTDESLFPVLKQLDAQQTQLRIDSFFRLAQQEKEDAKRIKSQRLNRAVTCMLRKEKEAAASEIEAVSVAM HUMXPG.PRO
336 KTDESLYPVLKHLNAHQTQLRIDSFFRLAQQEKQDAKLIKSHRLSRAVTCMLRKEREEKAPELTKVTEAM MUSXPG.PRO
336 KTDEVLLPVLKQLNAQQTQLRIDSFFRLEQHEAAG---LKSQRLRRAVTCMKRKERDVEAEEVEAAVAVM XENXPG.PRO
257 EIPARSEDTQRKLRLRRKKYNFPVGFPNCDAVHNAITMYLRPPVSSEIPKIIPR-----AANFQQVAEIM CELRAD2.PRO
```

FIG. 70C




```
314 ----------------------------------------------------------------------MJAFEN1.PRO
327 ----------------------------------------------------------------------PFUFEN1.PRO
348 ----------------------------------------------------------------GSLS HUMFEN1.PRO
346 ----------------------------------------------------------------GSLS MUSFEN1.PRO
351 ----------------------------------------------------------------PK-T YST510.PRO
357 KRINEFF----------------------------------------------------------- YSTRAD2.PRO
359 SNLTQFFEGGNTNVYAPRVAYHFKSKRLENALSSFKNQISNQSPMSEEIQADADAFGESKGSDELOSRIL SPORAD13.PRO
406 EKEFELLDKAKRKTQKRGITNTLEESSSLKRKRLSDSKRKNTCGGFLGETCLSESSDGSSSEHAESSSLM HUMXPG.PRO
406 EKEFELLDDAKGKTOKRELPYK-------KETSVPKRRRPSGNGGFLGDPYCSESPQESSCEDGEGSSVM MUSXPG.PRO
403 ERECTNQRKGQKTNTKS-------QGTKRRKPTECSQEDQDPGGGFIGIELKTLSSKAYSSD-------- XENXPG.PRO
322 MKECGWPATRTQKELALSIRRKVHLTTTVAQTRIPDFFAATKSKNFTPIVEPCESLEDYISANN-----T CELRAD2.PRO
```


```
314 ----------------------------------------------------------NKTKQKTL MJAFEN1.PRO
327 ----------------------------------------------------------KSGKQSTL PFUFEN1.PRO
352 SAKRKEPEPKGST-----------------------------------------------KKKAKTGAAG HUMFEN1.PRO
350 SAKRKEPEPKGPA-----------------------------------------------KKKAKTGGAG MUSFEN1.PRO
354 KEQLAAAAKRAQE-----------------------------------------------NKKLNKNKNK YST510.PRO
364 -------------------------PREYISGDKKLNTSKRISTATGKL---------------KK  YSTRAD2.PRO
429 RRKKMMASKNSSDSDSDSEDNFLASLTPKTNSSSISIENLPRKTKLSTSLL---------------KKP SPORAD13.PRO
476 NVQRRTAAKEPKTSASDSONSVKEAPVKNGGATTSSSSDSDDDGGKEKMVLVTARSVFGKKRRKLRRARG HUMXPG.PRO
469 SARQRSAAESSKIGCSDVPDLVRDSPHGRQGCVSTSSSDSEDGEDKAKTVLVTARPVFGKKRRKLKSMK- MUSXPG.PRO
458 -----GSSSDAEDLPSGLIDKQSQSGIVGROKASNKVESSSSSDDEDRTVMVTAKPVFQGKKTKSKTMKE XENXPG.PRO
387 WMRKRKRSESPQILQHHAKRQVPDRK--------------------------RSVKIRAFKPYPTDVI CELRAD2.PRO
```

FIG. 70D

322	DAWFKZ	MJAFEN1.PRO
335	ESWFKR	PFUFEN1.PRO
375	KFKRGK	HUMFEN1.PRO
373	KFRRGK	MUSFEN1.PRO
377	VTKGRR	YST510.PRO
390	---RKM	YSTRAD2.PRO
483	SKRRRK	SPORAD13.PRO
546	RKRKTZ	HUMXPG.PRO
538	RRKKKT	MUSXPG.PRO
523	TVKRK	XENXPG.PRO
429	ELGDSD	CELRAD2.PRO

FIG. 70E

EP 0 681 306 A2

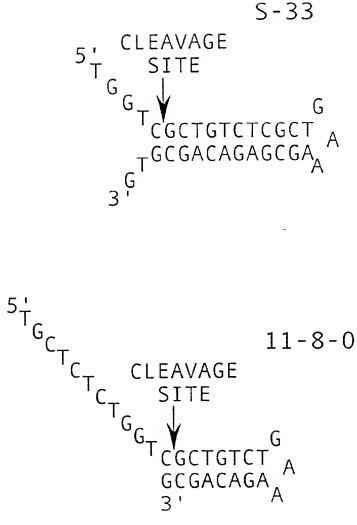


FIG. 71